

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Gruys, Kenneth J.

Mitsky, Timothy A.

Kishore, Ganesh M.

Slater, Steven C.

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Padgette, Stephen R.

Stark, David M.

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Connor-Ward, Dannette V.

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Rozman, Renee J.

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(ii) TITLE OF INVENTION: Methods of Optimizing Substrate Pools and Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalerate in Bacteria and Plants

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(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Gary M. Bond, Monsanto Company, A3SB

(B) STREET: 800 North Lindbergh Boulevard

(C) CITY: St. Louis

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(D) STATE: Missouri

(E) COUNTRY: USA

(F) ZIP: 63167

(v) COMPUTER READABLE FORM:

35

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

5 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 13-MAR-1996

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bond, Gary

(B) REGISTRATION NUMBER: 29,283

(C) REFERENCE/DOCKET NUMBER: 38-21(13585)A

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (314) 694-3412

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1545 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

35

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG

60

CTGCGCGCGC CGGTTTACGA GGCGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAAACTG

120

	TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGCACAGC	180
	TTTAAGCTGC CGGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACAA GAAAGCGCAC	240
5	GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTC TTCTGCGCGG	300
	TTAGGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG	360
10	CTGCGCGGCT TCGGCGGCGA AGTGCCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC	420
	AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG	480
	ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAACCTGC TCCAGCAGGA CGCCCATCTC	540
15	GACCGCGTAT TTGTGCCAGT CGGGCGCGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC	600
	AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG	660
20	AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA	720
	GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC	780
	GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGCGA TGAAGGATT ATTGAAAGAT	840
25	GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC	900
	GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC	960
30	TTCCACGGCC TGCCTACGT CTCAGAACGC TGCGAACTGG TCGAACAGCG TGAAGCGTTG	1020
	TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCTCA AATTCTGCCA ACTGCTTGGC	1080
	GGGCCTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTT	1140
35	GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTGCA GATGCTAAC	1200
	GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC	1260

TATATGGTCG	GCGGACGTCC	ATCGCATCCG	TTGCAGGAAC	GCCTCTACAG	CTTCGAATTC	1320	
5	CCGGAATCAC	CGGGCGCGCT	GCTGCGCTTC	CTCAACACGC	TGGGTACGTA	CTGGAACATT	1380
	TCTTTGTTCC	ACTATCGCAG	CCATGGCACC	GACTACGGGC	GCGTACTGGC	GGCGTTCGAA	1440
10	CTTGGCGACC	ATGAACCGGA	TTTCGAAACC	CGGCTGAATG	AGCTGGGCTA	CGATTGCCAC	1500
	GACGAAACCA	ATAACCCGGC	GTTCAGGTTC	TTTTTGGCGG	GTCAA		1545

(2) INFORMATION FOR SEQ ID NO:2:

5 (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 46 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA"

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTTTTGGATC	CGATATCTTA	ACCCGCCAAA	AAGAACCTGA	ACGCCG	46
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30 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTGGATC CATGGCTGAC TCGCAACCCC TGTCCGG

37

10 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CAGCTTCGAG TTCCCGGAAT CACCGGGCGC GTTCCTGCGC TTCC

44

(2) INFORMATION FOR SEQ ID NO:5:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: nucleic acid
- 35 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5	ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG	60
	CTGCGCGCGC CGGTTTACGA GGCGGCCAG GTTACGCCGC TACAAAAAAT GGAAAAACTG	120
	TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGCACAGC	180
10	TTTAAGCTGC CGGGCGATA CGCCATGATG GCGGGCCTGA CGGAAGAACAA GAAAGCGCAC	240
	GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTC TTCTGCGCGG	300
15	TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG	360
	CTGCGCGGCT TCGGCGCGA AGTGCCTGTC CACGGCGCGA ACTTGATGA AGCGAAACGC	420
	AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG	480
20	ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAACTGC TCCAGCAGGA CGCCCATCTC	540
	GACCGCGTAT TTGTGCCAGT CGGGCGCGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC	600
25	AAACAACGTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAACG CGGAAGACTC CGCCTGCCTG	660
	AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA	720
	GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC	780
30	GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGCGA TGAAGGATT ATTGAAAGAT	840
	GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC	900
35	GCCCTGCACA ACATTGCGGG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC	960
	TTCCACGGCC TCGCCTACGT CTCAGAACGC TCGGAACCTGG TCGAACAGCG TGAAGCGTTG	1020

	TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC	1080
	GGGCCTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT	1140
5	GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTGCA GATGCTAAC	1200
	GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC	1260
	TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAGTTC	1320
10	CCGGAATCAC CGGGCGCGTT CCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT	1380
	TCTTTGTTCC ACTATCGCAG CCATGGCACC GACTACGGGC GCGTACTGGC GGCGTTCGAA	1440
15	CTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC	1500
	GACGAAACCA ATAACCCGGC GTTCAGGTT TC TTTTGGCGG GTTAA	1545
	(2) INFORMATION FOR SEQ ID NO:6:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 65 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
	(A) DESCRIPTION: /desc = "synthetic DNA"	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
35	TATCGCAGCC ACGGCACCGA CTACGGCGC GTACTGGCGG CGTTCGAATT TGGCGACCAT	60
	GAACC	65

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 1545 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

15

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60

CTGCGCGCGC CGGTTTACGA GGCGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAAAATG 120

20

TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGCACAGC 180

TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACAA GAAAGCGCAC 240

GGCGTGATCA CTGCTTCTGC GGGTAACCCAC GCGCAGGGCG TCGCGTTTC TTCTGCGCGG 300

25

TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG 360

CTGCGCGGCT TCGGCGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC 420

30

AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG 480

ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAACCTGC TCCAGCAGGA CGCCCATCTC 540

GACCGCGTAT TTGTGCCAGT CGGCAGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC 600

35

AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG 660

AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA 720

	GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC	780
	GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGCGA TGAAGGATTT ATTGAAAGAT	840
5	GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAAATGAA AAAATATATC	900
	GCCCTGCACA ACATTGCGGG CGAACGGCTG GCGCATATTG TTTCCGGTGC CAACGTGAAC	960
10	TTCCACGGCC TGCGCTACGT CTCAGAACGC TGCGAACTGG TCGAACAGCG TGAAGCGTTG	1020
	TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC	1080
	GGGCGTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAACGC CTGCATCTT	1140
15	GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTGCA GATGCTAAC	1200
	GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC	1260
20	TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTGAATTG	1320
	CCGGAATCAC CGGGCGCGCT GCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT	1380
	TCTTTGTTCC ACTATCGCAG CCACGGCACC GACTACGGGC GCGTACTGGC GGCCTTCGAA	1440
25	TTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC	1500
	GACGAAACCA ATAACCCGGC GTTCAGGTTTC TTTTGGCGG GTTAA	1545
30	(2) INFORMATION FOR SEQ ID NO:8:	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG	60
	CTGCGCGCGC CGGTTTACGA GGCGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAAACTG	120
10	TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATGCCAGCC AGTGCACAGC	180
	TTTAAGCTGC GCGGCGCATA CGCCATGATG GCAGGGCTGA CGGAAGAACAA GAAAGCGCAC	240
15	GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTC TTCTGCGCGG	300
	TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG	360
	CTGCGCGGCT TCGGCGGCGA AGTGCCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC	420
20	AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG	480
	ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAACTGC TCCAGCAGGA CGCCCATCTC	540
25	GACCGCGTAT TTGTGCCAGT CGGGCGCGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC	600
	AAACAACGTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG	660
	AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA	720
30	GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCGTT TATGCCAGGA GTATCTCGAC	780
	GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGCGA TGAAGGATT ATTGAAAGAT	840
35	GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC	900
	GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC	960

TTCCACGGCC TGCCTACGT CTCAGAACGC TGCGAACTGG TCGAACAGCG TGAAGCGTTG 1020

TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC 1080

5 GGGCGTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTT 1140

GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGGCCAAAG AAATTTGCA GATGCTAAC 1200

GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC 1260

10 TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAGTTC 1320

CCGGAATCAC CGGGCGCGTT CCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380

15 TCTTTGTTCC ACTATCGCAG CCACGGCACC GACTACGGC GCGTACTGGC GGCGTTCGAA 1440

TTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500

GACGAAACCA ATAACCCGGC GTTCAGGTT TC TTTTGGCGG GTTAA 1545

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 1185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGACGCGTG AAGTGGTAGT GGTAAGCGGT GTCCGTACCG CGATCGGGAC CTTTGGCGGC 60

	AGCCTGAAGG ATGTGGCACC GGCGGAGCTG GGCGCACTGG TGGTGCAGCA GGCCTGGCG	120
	CGCGCGCAGG TGTGGGCGA CGATGTCGGC CACGTGGTAT TCGGCAACGT GATCCAGACC	180
5	GAGCCGCGCG ACATGTATCT GGGCCGCGTC GCGGCCGTCA ACGGCGGGT GACGATCAAC	240
	GCCCCCGCGC TGACCGTGAA CCGCCTGTGC GGCTCGGGCC TGCAGGCCAT TGTCAGCGCC	300
	GCGCAGACCA TCCTGCTGGG CGATACCGAC GTGCCATCG GCGGCCGGCG GGAAAGCATG	360
10	AGCCCGCGAC CGTACCTGGC CCCGGCAGCG CGCTGGGGCG CACGCATGGG CGACGCCGGC	420
	CTGGTCGACA TGATGCTGGG TGCCTGCAC GATCCCTTCC ATGCATCCA CATGGCGTG	480
15	ACCGCCGAGA ATGTCGCCAA GGAATACGAC ATCTCGCGCG CGCAGCAGGA CGAGGCCCG	540
	CTGGAATCGC ACCGCCGCGC TTCGGCAGCG ATCAAGGCCG GCTACTTCAA GGACCAGATC	600
	GTCCCCGGTGG TGAGCAAGGG CCGCAAGGGC GACGTGACCT TCGACACCGA CGACCACGTG	660
20	CGCCATGACG CCACCATCGA CGACATGACC AAGCTCAGGC CGGTCTTCGT CAAGGAAAAC	720
	GGCACGGTCA CGGCCGGCAA TGCCTCGGGC CTGAACGACG CGGCCGCCGC GGTGGTGATG	780
25	ATGGAGCGCG CCGAAGCCGA CGGCCGCGGC CTGAAGCCGC TGGCCCGCCT GGTGTCGTAC	840
	GGCCATGCCG GCGTGGACCC GAAGGCCATG GGCATCGGCC CGGTGCCGGC GACGAAGATC	900
	GCGCTGGAGC GCGCCGGCCT GCAGGTGTCG GACCTGGACG TGATCGAAGC CAACGAAGCC	960
30	TTTGCCGCAC AGGCGTGCAC CGTGACCAAG GCGCTCGGT TGGACCCGGC CAAGGTTAAC	1020
	CCGAACGGCT CGGGCATCTC GCTGGGCCAC CCGATCGCGC CCACCGGTGC CCTGATCACG	1080
35	GTGAAGGCAC TGCATGAGCT GAACCGCGTG CAGGGCCGCT ACGCGCTGGT GACGATGTGC	1140
	ATCGGCGGCG GGCAGGGCAT TGCCGCCATC TTGAGCGTA TCTGA	1185

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20 Thr Arg Glu Val Val Val Val Ser Gly Val Arg Thr Ala Ile Gly
1 5 10 15

25 (2) INFORMATION FOR SEQ ID NO:11:

20 (i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Thr Arg Glu Val Val Val Val Ser Gly Val Arg Thr Ala Ile Gly
35 1 5 10 15

30 Thr Phe Gly Gly Ser Leu Lys Asp Val Ala Pro Ala Glu Leu Gly Ala
20 25 30

Leu Val Val Arg Glu Ala Leu Ala Arg Ala Gln Val Ser Gly Asp Asp
 35 40 45

5 Val Gly His Val Val Phe Gly Asn Val Ile Gln Thr Glu Pro Arg Asp
 50 55 60

Met Tyr Leu Gly Arg Val Ala Ala Val Asn Gly Gly Val Thr Ile Asn
 65 70 75 80

10 Ala Pro Ala Leu Thr Val Asn Arg Leu Cys Gly Ser Gly Leu Gln Ala
 85 90 95

Ile Val Ser Ala Ala Gln Thr Ile Leu Leu Gly Asp Thr Asp Val Ala
 15 100 105 110

Ile Gly Gly Gly Ala Glu Ser Met Ser Arg Ala Pro Tyr Leu Ala Pro
 115 120 125

20 Ala Ala Arg Trp Gly Ala Arg Met Gly Asp Ala Gly Leu Val Asp Met
 130 135 140

Met Leu Gly Ala Leu His Asp Pro Phe His Arg Ile His Met Gly Val
 145 150 155 160

25 Thr Ala Glu Asn Val Ala Lys Glu Tyr Asp Ile Ser Arg Ala Gln Gln
 165 170 175

Asp Glu Ala Ala Leu Glu Ser His Arg Arg Ala Ser Ala Ala Ile Lys
 30 180 185 190

Ala Gly Tyr Phe Lys Asp Gln Ile Val Pro Val Val Ser Lys Gly Arg
 195 200 205

35 Lys Gly Asp Val Thr Phe Asp Thr Asp Glu His Val Arg His Asp Ala
 210 215 220

Thr Ile Asp Asp Met Thr Lys Leu Arg Pro Val Phe Val Lys Glu Asn

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230

235

240

Gly Thr Val Thr Ala Gly Asn Ala Ser Gly Leu Asn Asp Ala Ala Ala
245 250 255

5

Ala Val Val Met Met Glu Arg Ala Glu Ala Glu Arg Arg Gly Leu Lys
260 265 270

10

Pro Leu Ala Arg Leu Val Ser Tyr Gly His Ala Gly Val Asp Pro Lys
275 280 285

Ala Met Gly Ile Gly Pro Val Pro Ala Thr Lys Ile Ala Leu Glu Arg
290 295 300

15

Ala Gly Leu Gln Val Ser Asp Leu Asp Val Ile Glu Ala Asn Glu Ala
305 310 315 320

Phe Ala Ala Gln Ala Cys Ala Val Thr Lys Ala Leu Gly Leu Asp Pro
325 330 335

20

Ala Lys Val Asn Pro Asn Gly Ser Gly Ile Ser Leu Gly His Pro Ile
340 345 350

25

Gly Ala Thr Gly Ala Leu Ile Thr Val Lys Ala Leu His Glu Leu Asn
355 360 365

Arg Val Gln Gly Arg Tyr Ala Leu Val Thr Met Cys Ile Gly Gly Gly
370 375 380

30

Gln Gly Ile Ala Ala Ile Phe Glu Arg Ile
385 390